

FIG. 1

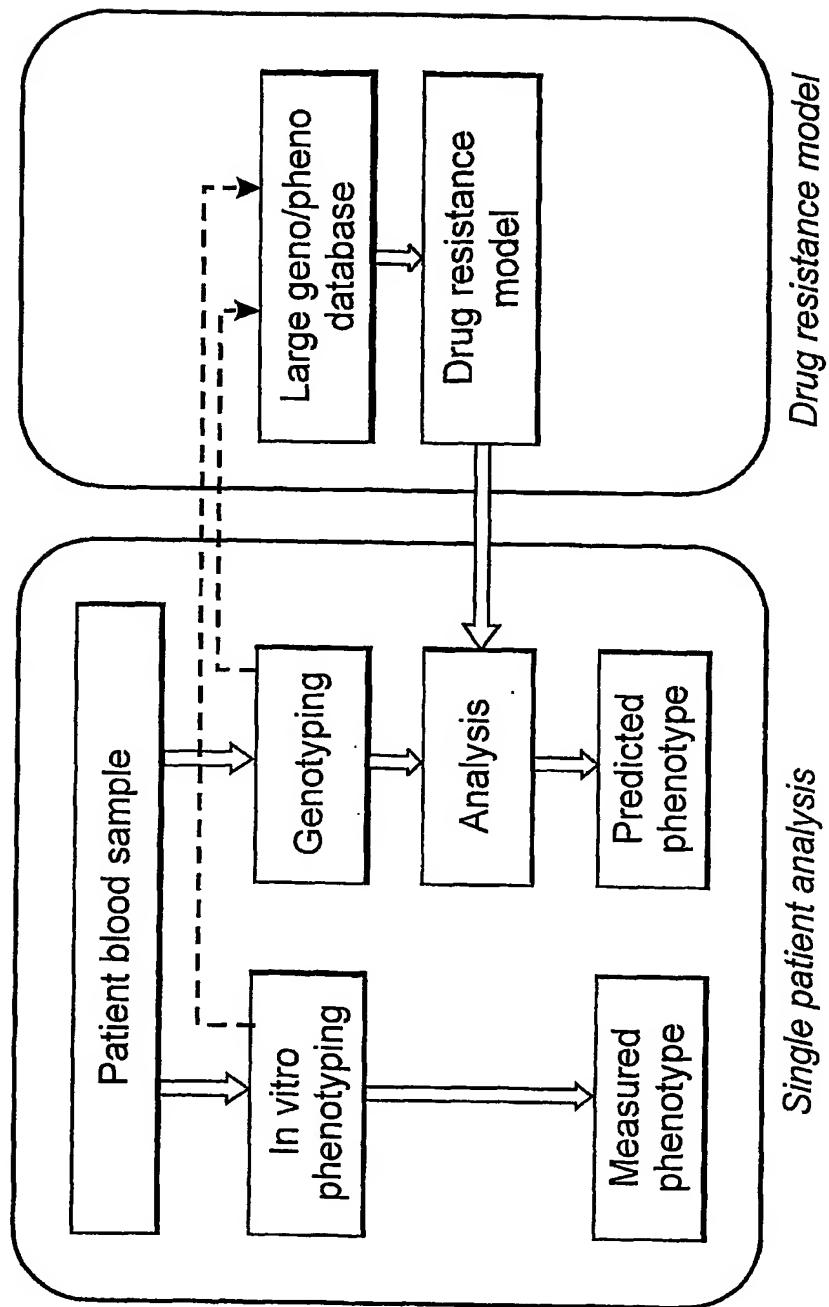


FIG. 2

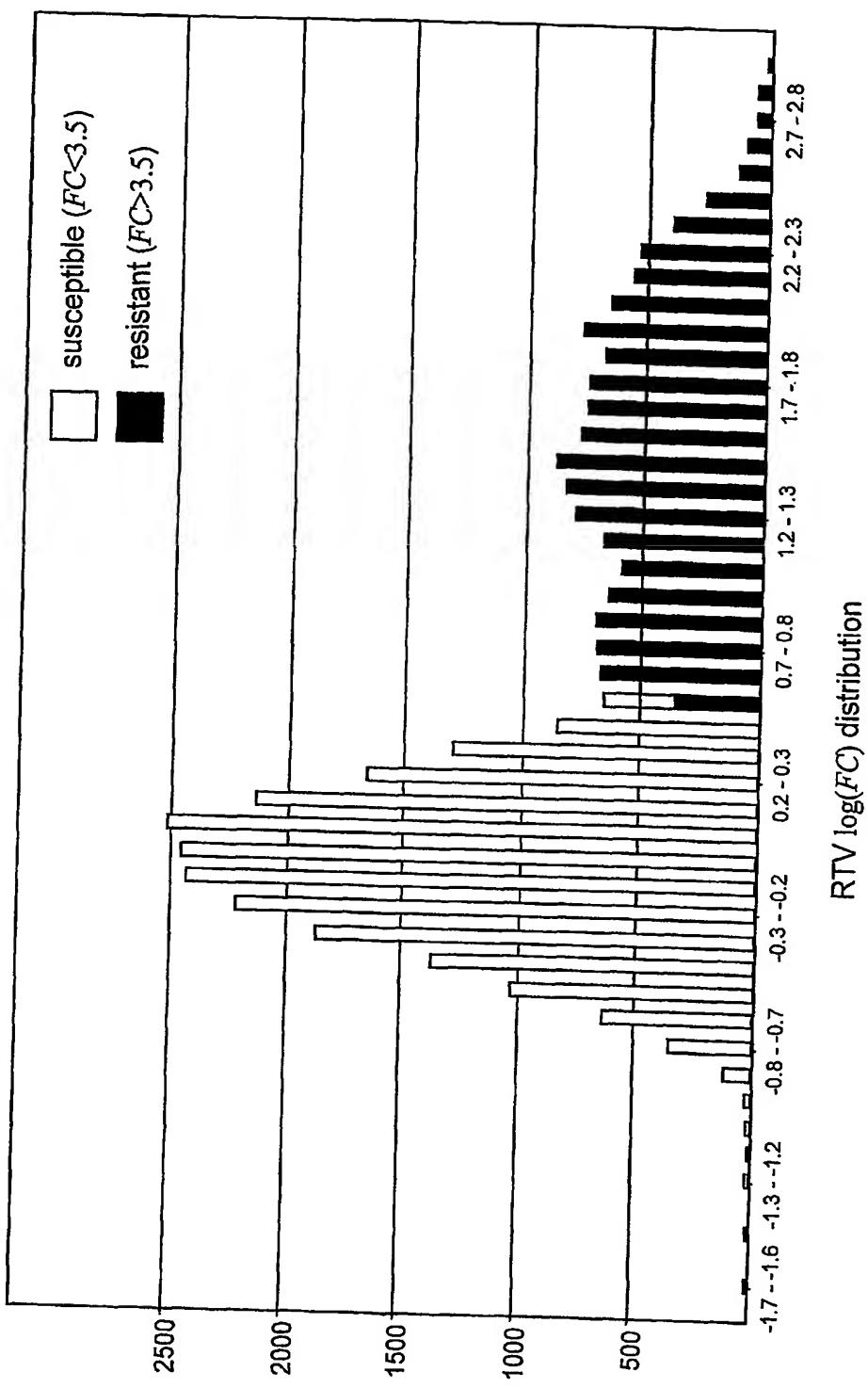


FIG. 3

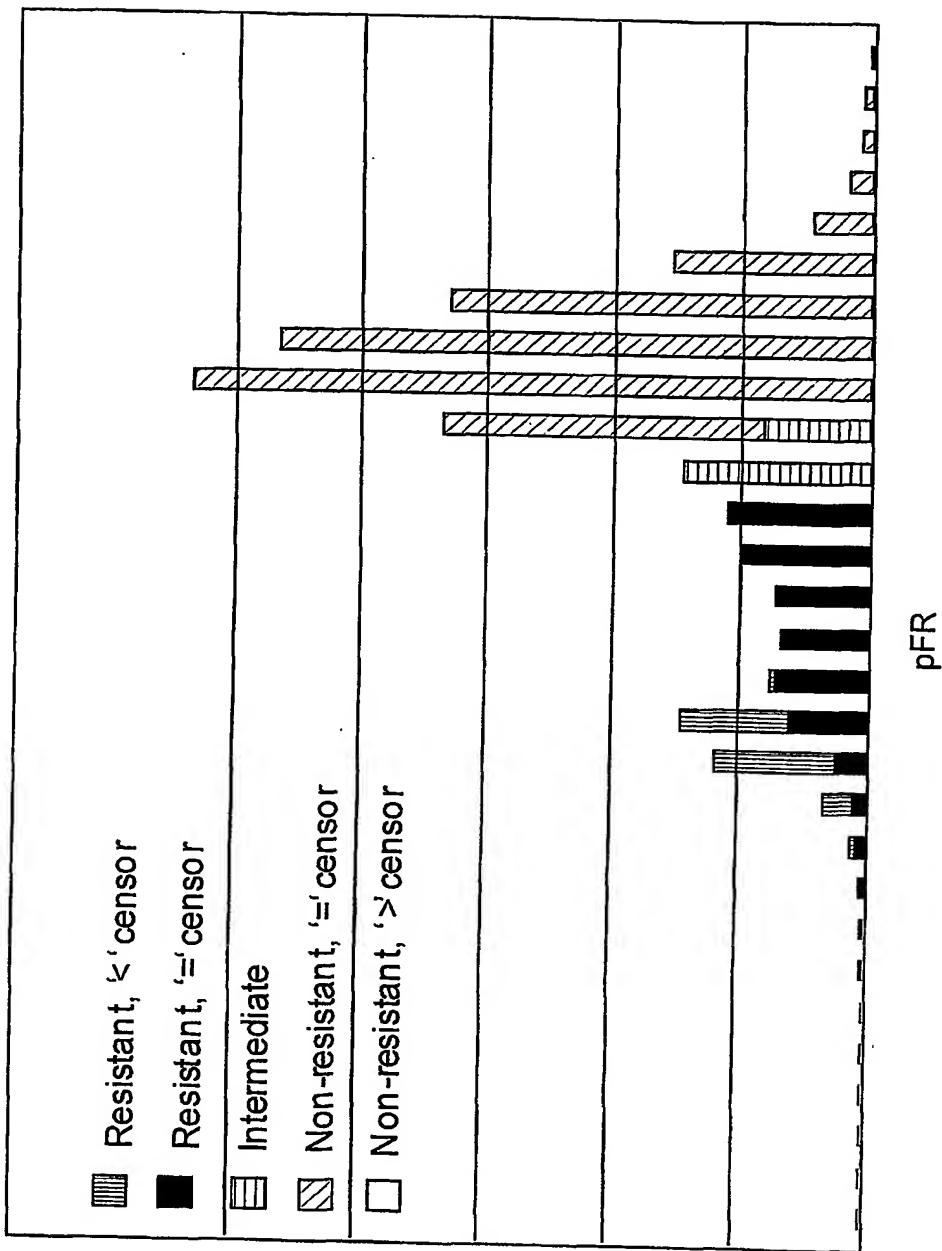


FIG. 4

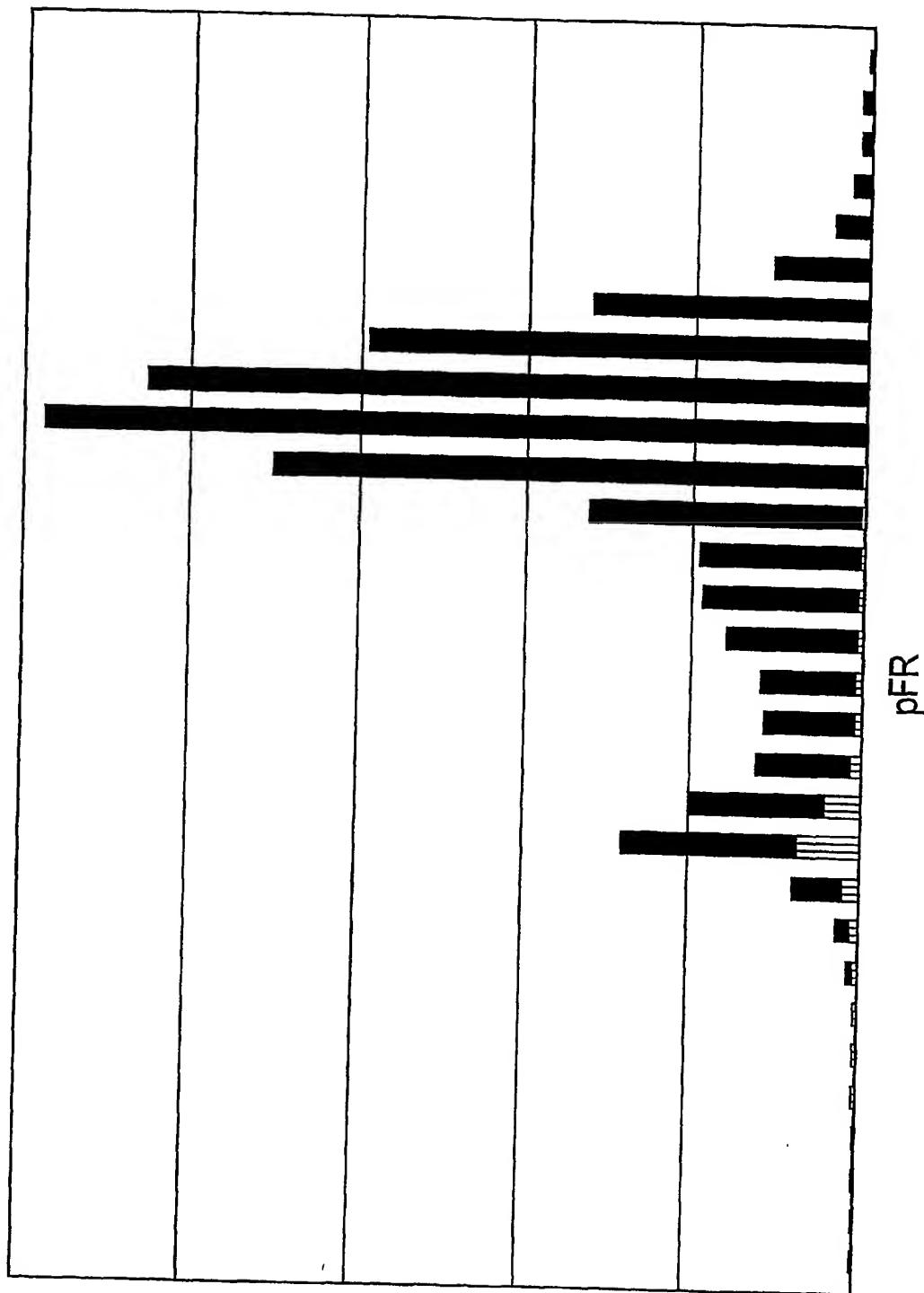


FIG. 5

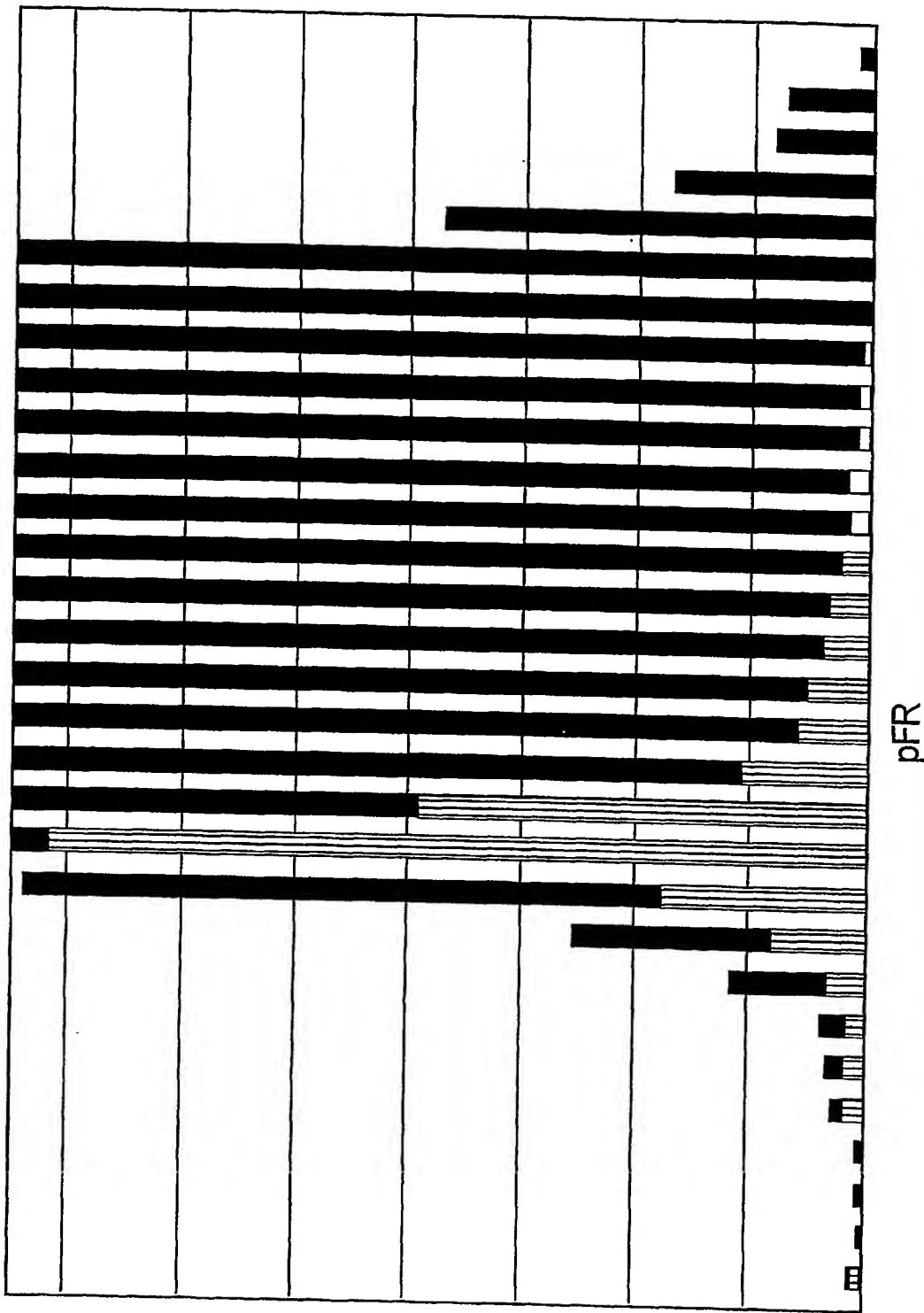


FIG. 6

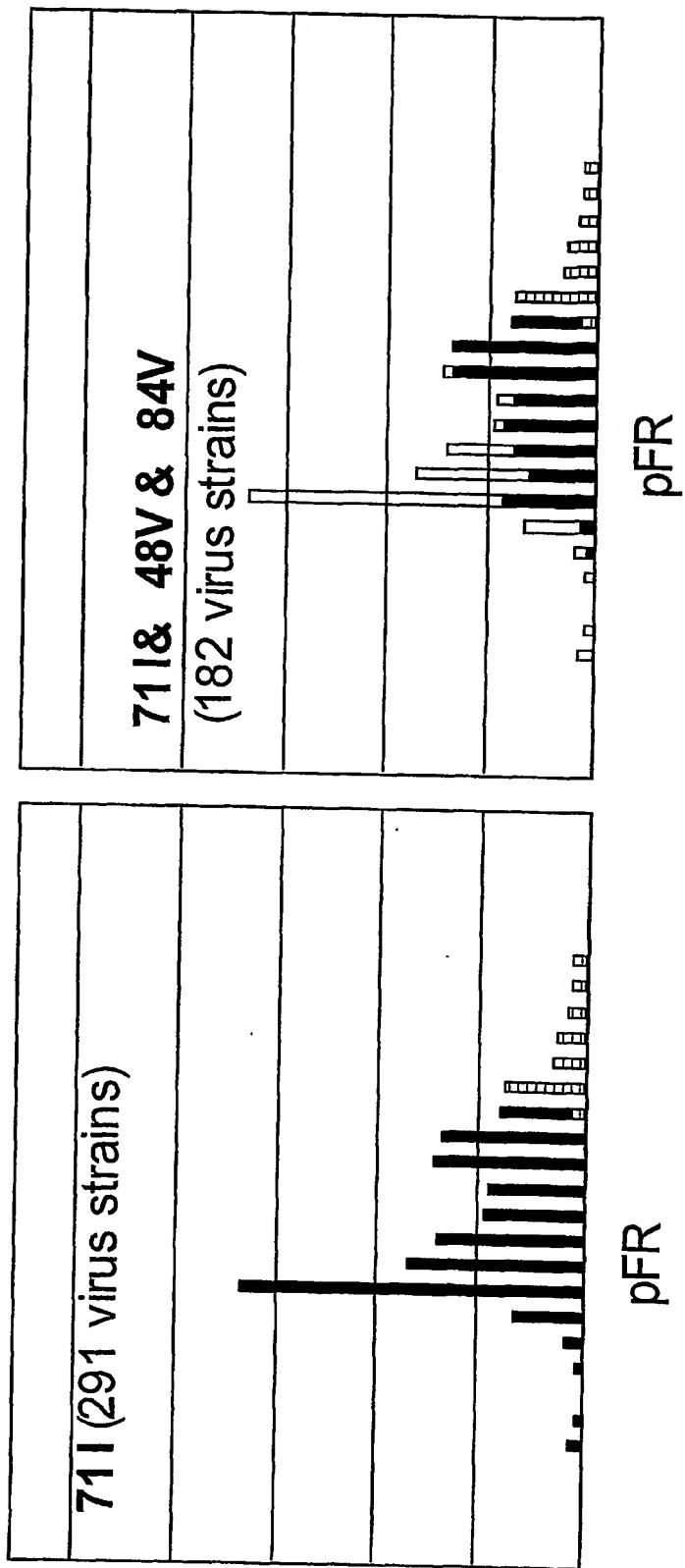


FIG. 7

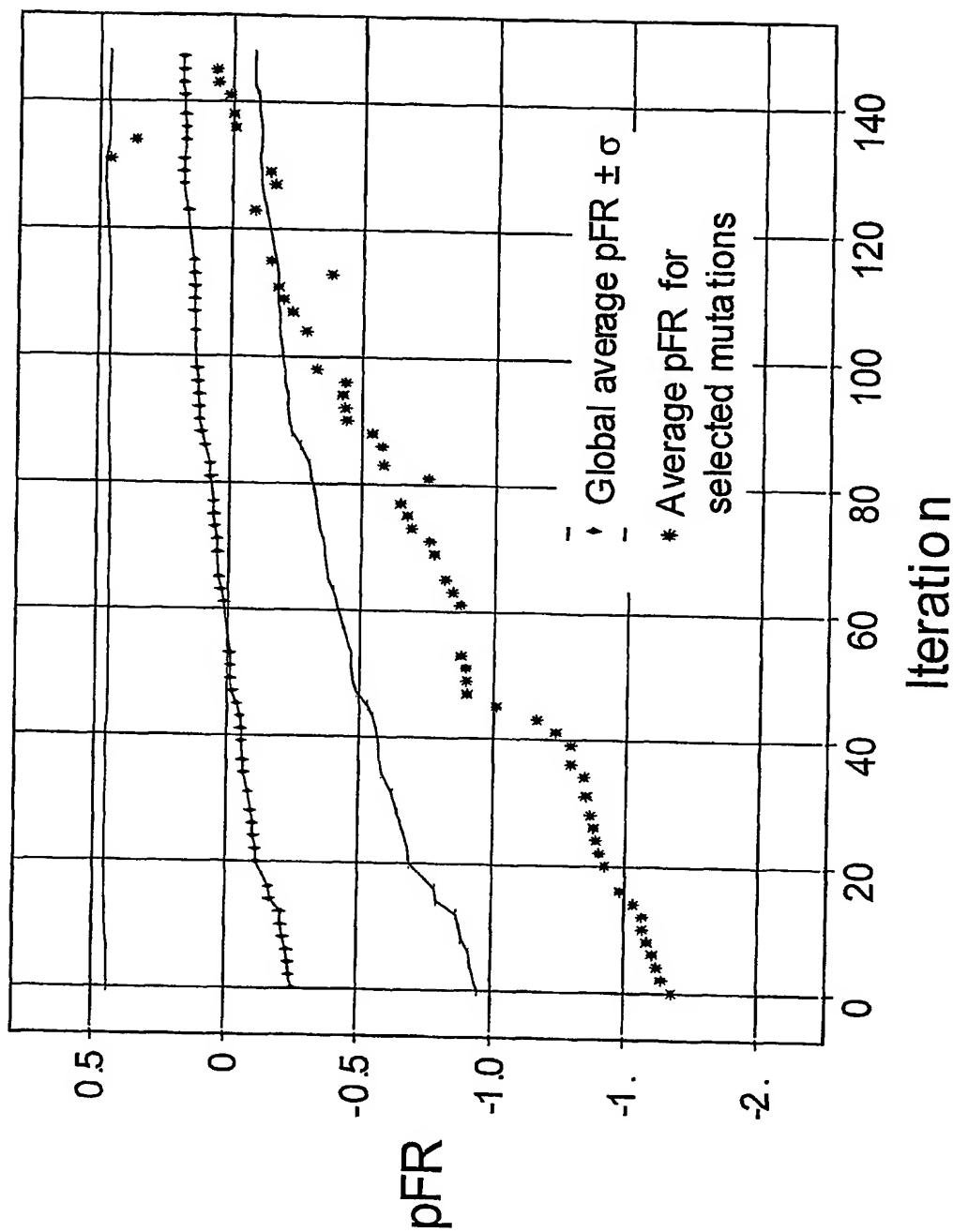


FIG. 8

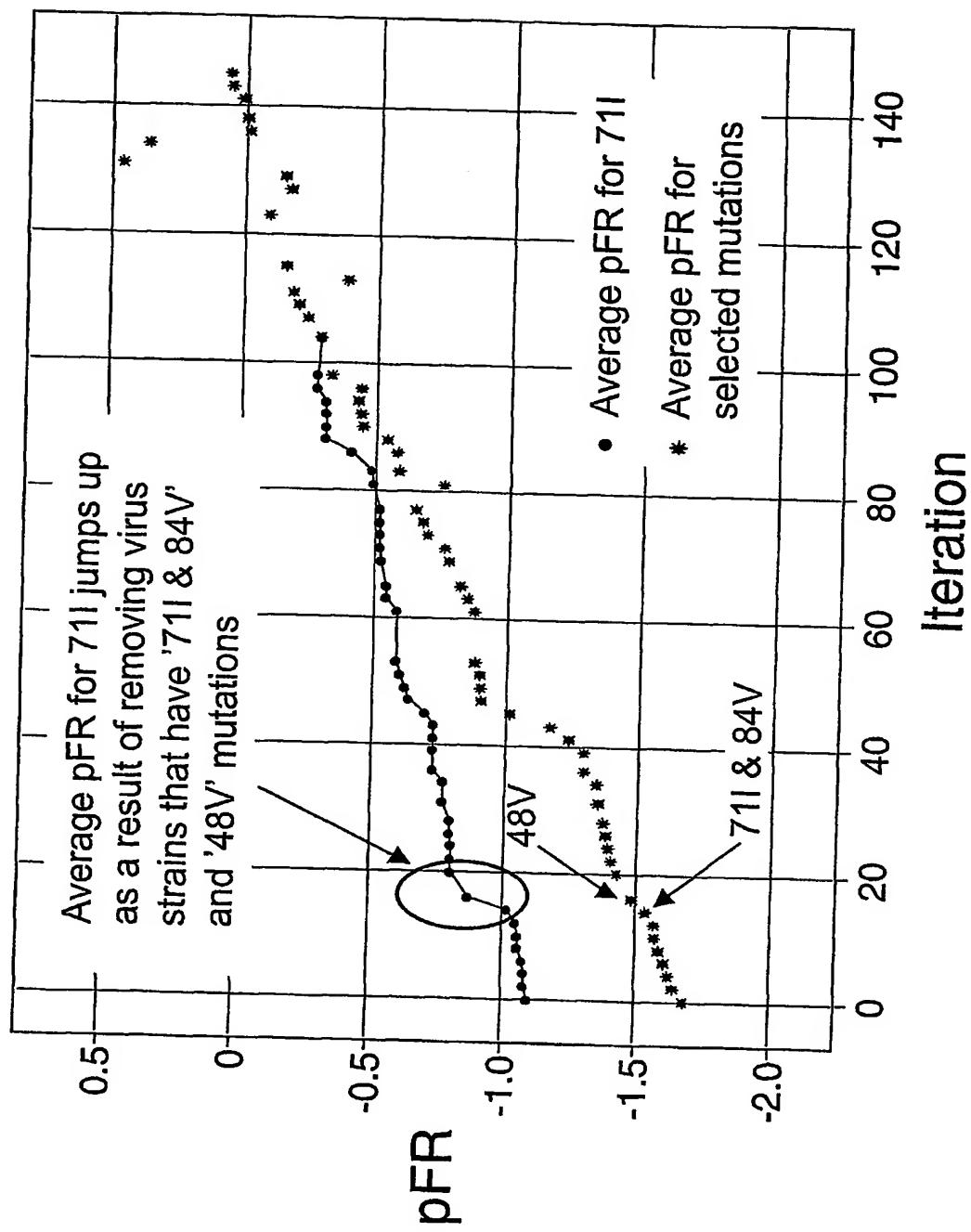


FIG. 9

Sample	Position																							
	3	10	12	15	19	20	24	30	32	36	37	41	46	48	54	62	63	71	74	75	77	82	84	93
V1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	A	L	A	L	A	L
V2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	V	A	-	-	-	-
V3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	P	-	-	-	-	-
V4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	W	P	V	-	-	T	W

FIG. 10

Offerer	Offer	Virus sample			Offer interactions
		V1	V2	V3	
Matched	0.50	0.39	0.32	1	-0.14
24	0.50	0.39	0.32	1	0.22
30V	0.50	0.39	0.32	1	-0.17
32	0.50	0.39	0.32	1	-0.17
46	0.50	0.39	0.32	1	-0.17
54T	0.52	0.33	0.21	1	-0.17
54V	0.52	0.33	0.21	1	-0.17
82A	0.63	0.52	0.39	1	-0.17
82T	0.59	0.47	0.36	1	-0.17
84V	0.67	0.57	0.47	1	-0.17
Offer interactions		-0.14	0.22	-0.17	-0.02
predicted log(FO)		0.86	2.18	0.56	7.77
measured log(FO)		0.89	2.15	0.59	8.1

FIG. 11

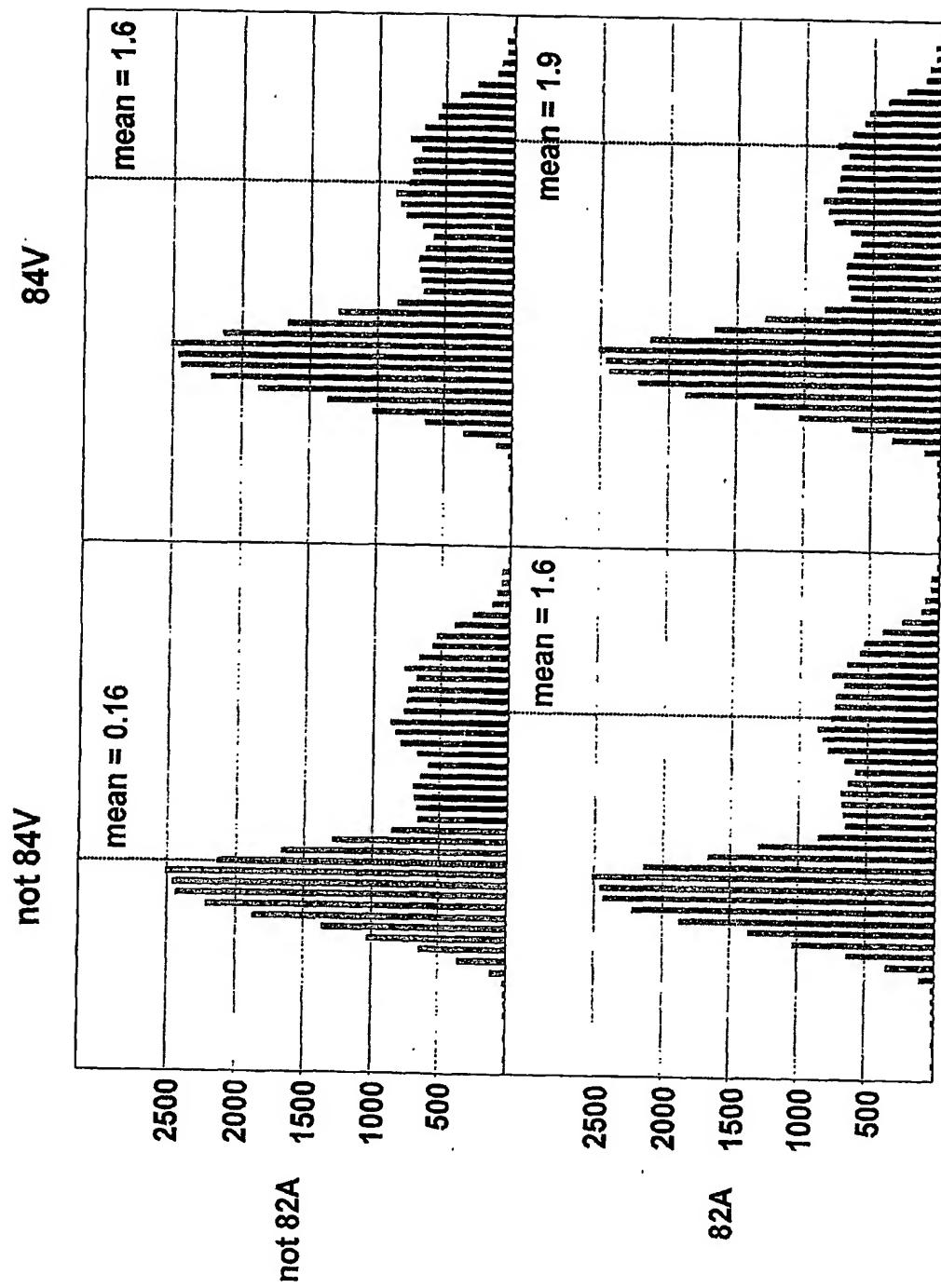


FIG. 12

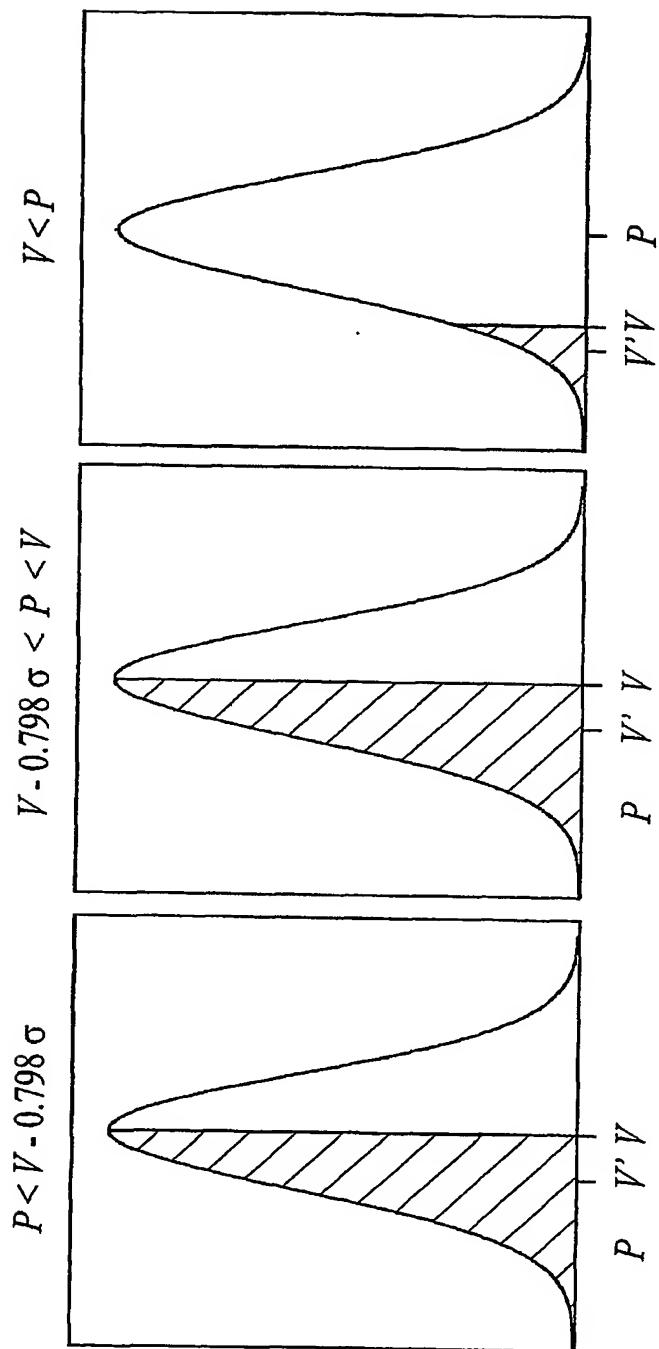


FIG. 13

Mutation	$1^{\text{st}}$ order log(FQ) shift	Prevalence in dataset
10*	$2^{\text{nd}}$ order items only	9,707
10R	0.35	106
10V	0.15	1,269
20H	$2^{\text{nd}}$ order items only	436
20R	$2^{\text{nd}}$ order items only	2,093
32	0.32	845
33F*	$2^{\text{nd}}$ order items only	1,074
36*	$2^{\text{nd}}$ order items only	8,473
46L	$2^{\text{nd}}$ order items only	4,115
54L	0.21	1,745
54V*	0.19	367
71T	0.33	4,553
71V	0.52	2,611
82A*	$2^{\text{nd}}$ order items only	7,261
82F	$2^{\text{nd}}$ order items only	4,886
82T*	0.63	290
82S	0.92	642
84V	0.58	120
90M	1.17	3,558
	0.67	9,609
	0.38	

FIG. 14

Mutation	$\log_2(F_0)$ shift	Prevalence in dataset
24	0.50	1,027
30N	-0.39	1,715
54T	1.33	155
73C	0.45	357
73S	0.38	2,224
73T	0.53	559
82M	0.66	33
84A	1.73	70
84C	0.79	67

FIG. 15

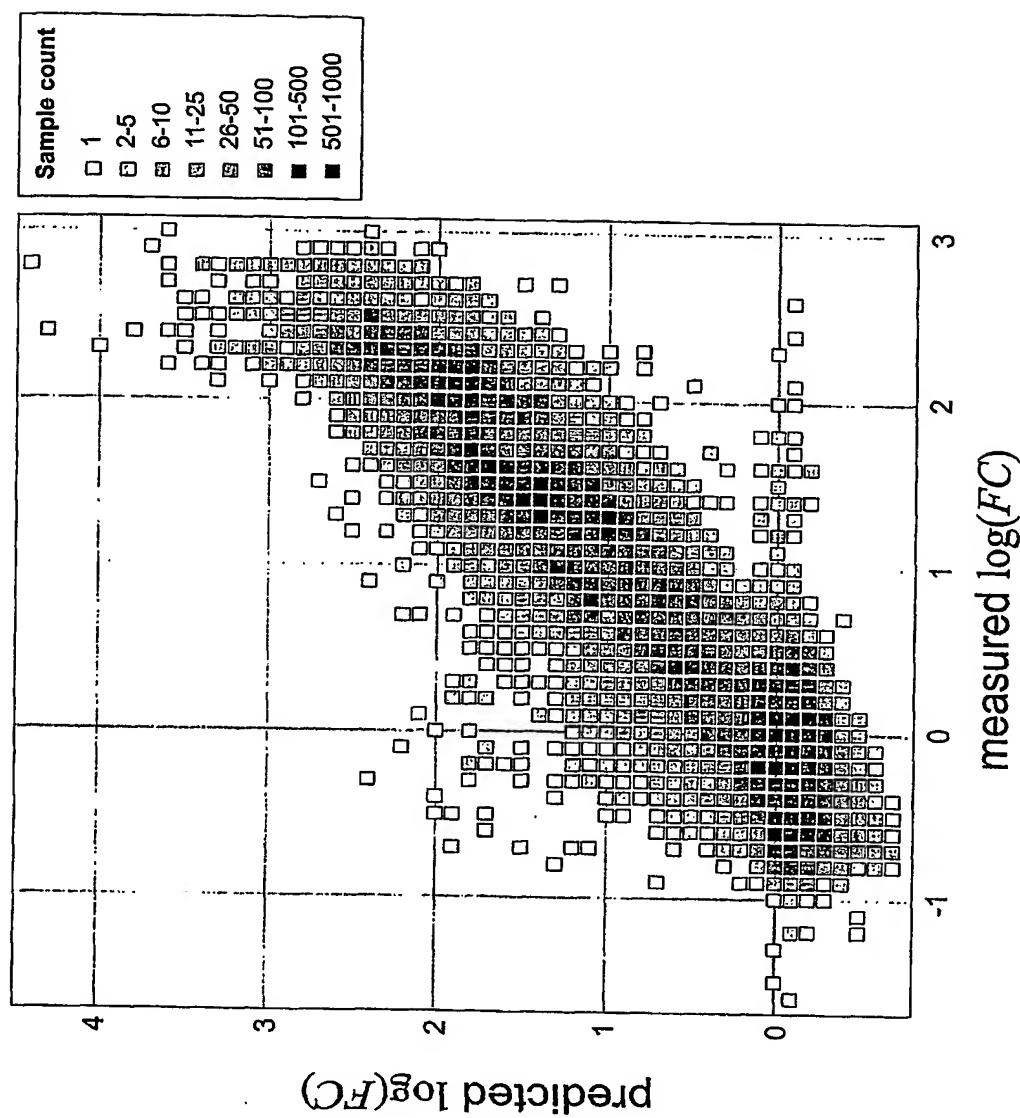


FIG. 16

	Nr. of samples	Resistant fraction (FC>3.5)	Leave-one-out prediction error	Sensitivity	Specificity
Decision tree	469	50.1%	10.2%	89.8%	89.7%
Linear model	469	50.1%	6.4%	92.9%	94.4%
Linear model	34,502	38.3%	5.6%	93.0%	95.4%

- Regression model identifies 53 single mutations and 96 pairs of mutations as having a positive or negative contribution to RTV susceptibility
- 20 out of 22 mutations from IAS list<sup>(1)</sup> are confirmed to be significant by regression model

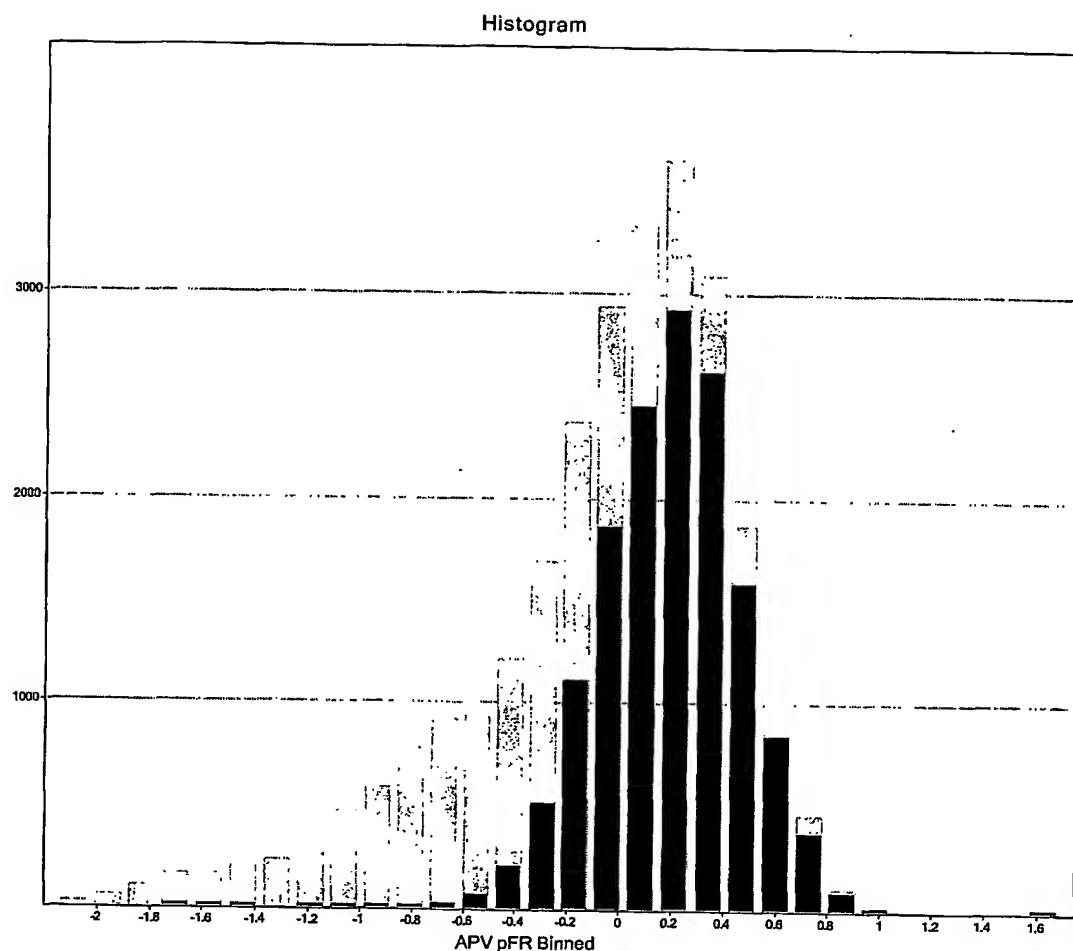


FIG. 17

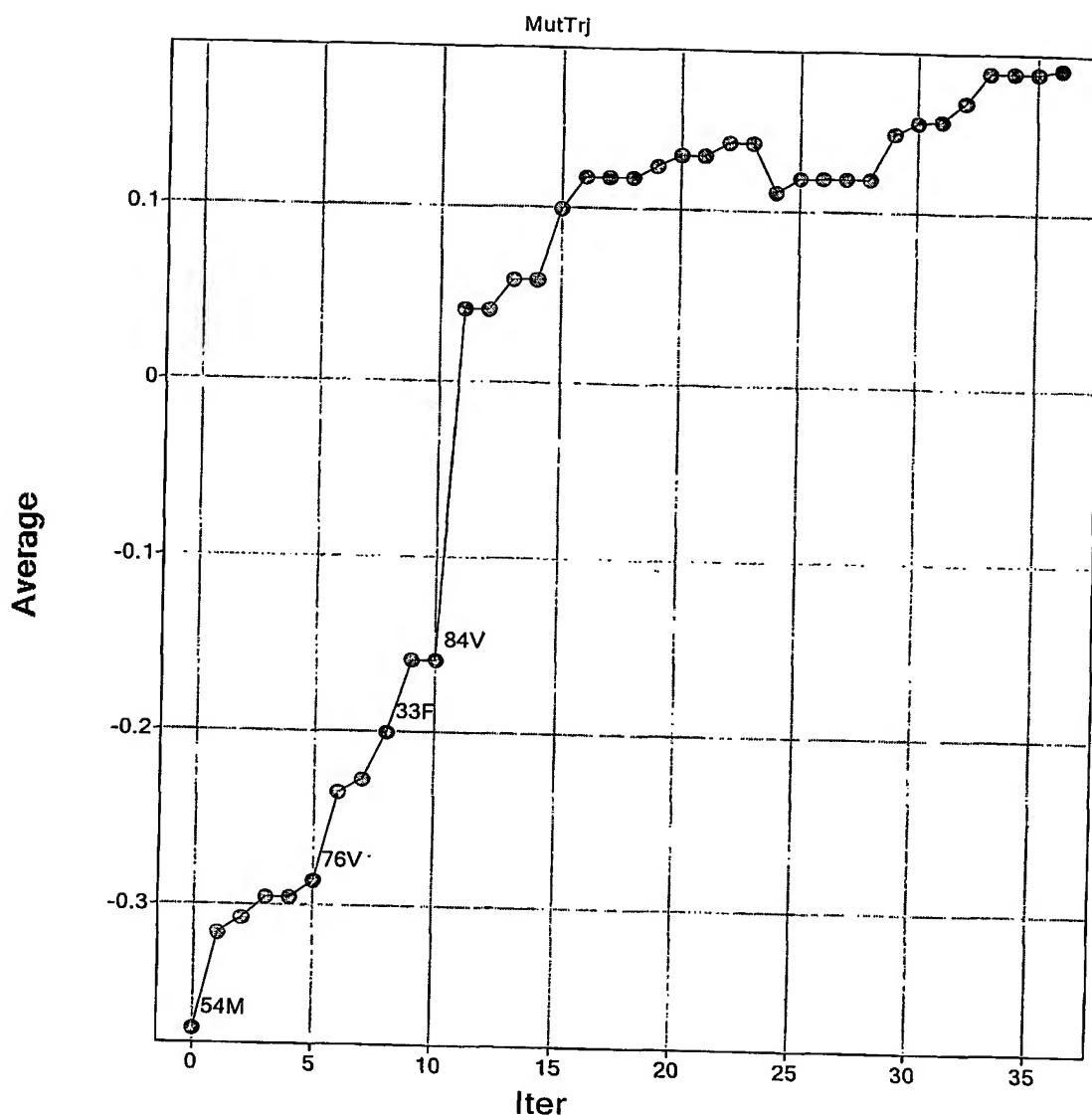


FIG. 18

Scatter Plot

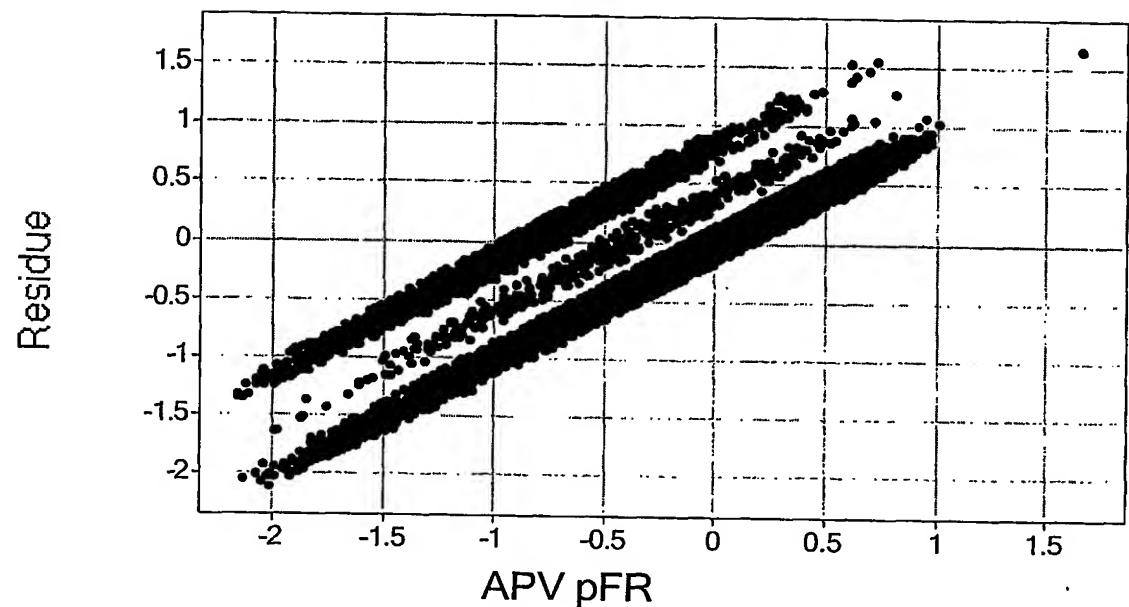


FIG. 19

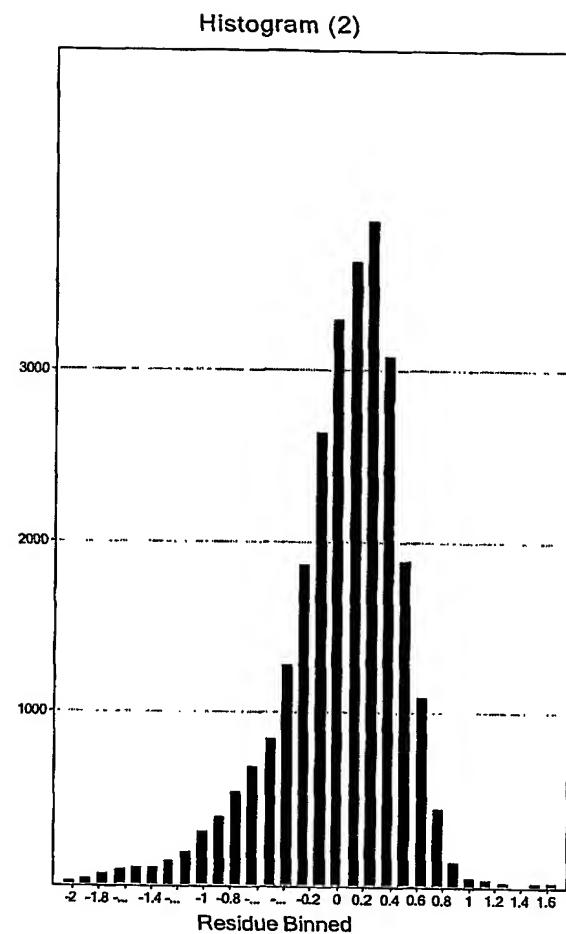
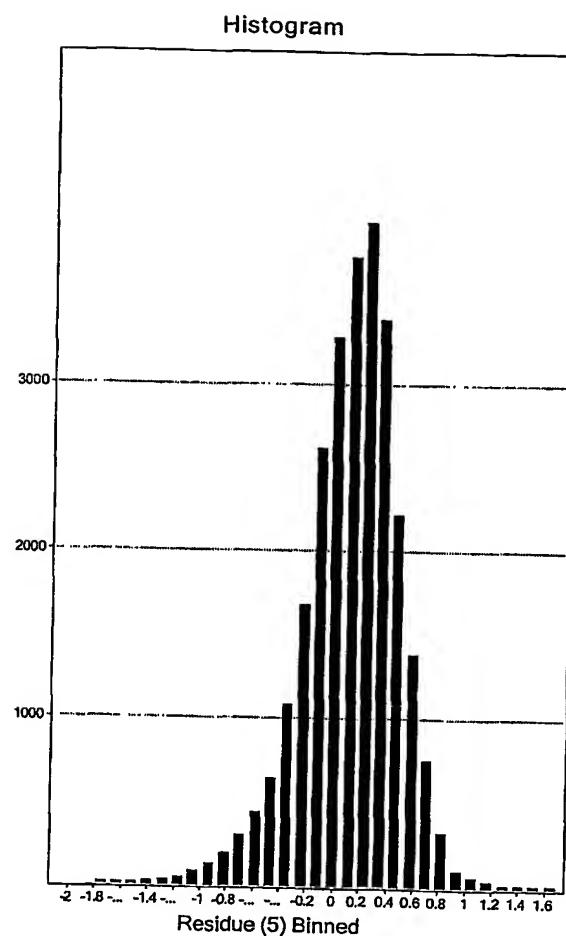


FIG. 20



**FIG. 21**